

RAW SEQUENCE LISTING

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Application Serial Number: 10/580,596
Source: IFWP
Date Processed by STIC: 06/07/2006

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IFWP

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DATE: 06/07/2006

PATENT APPLICATION: US/10/580,596

TIME: 11:02:16

Input Set : A:\70325USPCT Seq List.ST25.txt

Output Set: N:\CRF4\06072006\J580596.raw

3 <110> APPLICANT: SYNGENTA PARTICIPATIONS AG
 4 NEGROTTO, David V.
 5 SHOTKOSKI, Frank A.
 6 YU, Wenjin A.
 8 <120> TITLE OF INVENTION: INSECT RESISTANT COTTON PLANTS AND METHODS OF DETECTING THE
 SAME
 10 <130> FILE REFERENCE: 70325USPCT
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/580,596
 C--> 12 <141> CURRENT FILING DATE: 2006-05-25
 12 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/012662
 13 <151> PRIOR FILING DATE: 2004-11-09
 15 <150> PRIOR APPLICATION NUMBER: US 60/526,112
 16 <151> PRIOR FILING DATE: 2003-12-01
 18 <160> NUMBER OF SEQ ID NOS: 18
 20 <170> SOFTWARE: PatentIn version 3.2
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 26
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: COT202 nucleotide motif
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 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 26
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence
 39 <220> FEATURE:
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 43 ttcccgctt cagattttct gcaaca 26
 46 <210> SEQ ID NO: 3
 47 <211> LENGTH: 23
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
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 58 <210> SEQ ID NO: 4
 59 <211> LENGTH: 24
 60 <212> TYPE: DNA
 61 <213> ORGANISM: Artificial Sequence
 63 <220> FEATURE:

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73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
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83 <211> LENGTH: 20
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
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107 aagatcgact tcaccaagaa gatgaagacc ctgcgtacg aggtgaccgc caacttctac    180
109 gacagcagca cgggcgagat cgacctgaac aagaagaagg tggagagcag cgaggccgag    240
111 taccgcaccc tgagcgcgaa cgacgacggc gtctacatgc cactggggcgt          290
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127 aaaaatcctg aacatcttat tttagcaaag agaaagagtt ccgagtctgt agcagaagag    180
129 tgaggagaaa tttaagctct tggacttgtg aattgttccg cctcttgaat acttcttcaa    240
131 tcctcatata ttcttcttct atgttacctg aaaaccggca ttaaatctcg cgggtttatt    300
133 ccggttcaac attttttttg ttttgagtta ttatctgggc ttaataacgc aggcctgaaa    360
135 taaattcaag gcccaactgt tttttttttt aagaagttgc tgttaaaaaa aaaaaaaggg    420
137 aattaacaac aacaacaaaa aaagataaag aaaataataa caattacttt aattgtagac    480
139 taaaaaaaaca tagattttat catgaaaaaa agagaaaaaa aataaaaaact tggatcaaaa    540
141 aaaaacatac agatcttcta attattaact tttcttaaaa attaggtcct tttcccaac    600
143 aattaggttt agagtttttg aattaaacca aaaagattgt tctaaaaaat actcaaattt    660

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147	ttagagtaga	ttagaatctt	ttatgccaa	tattgataaa	ttaaatacaag	aagataaact	780
149	atcataatca	acatgaaatt	aaaagaaaaa	tctcatatat	agtattagta	ttctctatat	840
151	atattatgat	tgcttattct	taatgggttg	ggttaaccaa	gacatagtct	taatggaaag	900
153	aatctttttt	gaactttttc	cttattgatt	aaattcttct	atagaaaaga	aagaaattat	960
155	ttgaggaaaa	gtatatacaa	aaagaaaaat	agaaaaatgt	cagtgaagca	gatgtaatgg	1020
157	atgacctaat	ccaaccacca	ccataggatg	tttctacttg	agtcggtctt	ttaaaaacgc	1080
159	acggtgga	atatgacacg	tatcatatga	ttccttcctt	tagtttcctg	ataataatcc	1140
161	tcaactgata	tcttcctttt	tttggttttg	ctaaagatat	tttattctca	ttaatagaaa	1200
163	agacggtttt	gggctttttg	tttgcgatat	aaagaagacc	ttcgtgtgga	agataataat	1260
165	tcatectttc	gtctttttct	gactcttcaa	tctctcccaa	agcctaaagc	gatctctgca	1320
167	aatctctcgc	gactctctct	ttcaaggat	atcttctgat	tctttttgtt	tttgattcgt	1380
169	aatctgatct	caatttttgt	tatgtggatt	attgaattct	ttgtataaat	tgcttttgac	1440
171	aatattgttc	gtttcgtcaa	tccagctctc	aaattttgtc	ctgattacta	agatattcgt	1500
173	tcgtagtgtt	tacatctgtg	taatttcttg	cttgattgtg	aaattaggat	tttcaaggac	1560
175	gatctattca	atcttttgtt	tttctttgtt	cgattctctc	tgtttttaggt	ttcttatgtt	1620
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183	ctacggcttc	gccaccggca	tcaaggacat	catgaacatg	atcttcaaga	ccgacaccgg	1860
185	cggcgacctg	accctggacg	agatcctgaa	gaaccagcag	ctgctgaacg	acatcagcgg	1920
187	caagctggac	ggcgtgaacg	gcagcctgaa	cgacctgatc	gccaggggca	acctgaacac	1980
189	cgagctgagc	aaggagatcc	ttaagatcgc	caacgagcag	aaccagggtg	tgaacgacgt	2040
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217	caacgacagc	atcaccgtgc	tgaagggtga	cgaggccaag	ctgaagcaga	actaccaggt	2880
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229	gaccttcttg	accccgatca	acggcttttg	cctgcaggcc	gacgagaaca	gccgcctgat	3240
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233	ggagaccaag	ctgatcgtgc	caccgagcgg	cttcatcagc	aacatcgtgg	agaacggcag	3360
235	catcgaggag	gacaacctgg	agcgtgggaa	ggccaacaac	aagaacgcct	acgtggacca	3420
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239	gttcatcggc	gacaagctga	agccgaagac	cgagtacgtg	atccagtaca	ccgtgaaggg	3540
241	caagccatcg	attcacctga	aggacgagaa	caccggctac	atccactacg	aggacaccaa	3600

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243 caacaacctg gaggactacc agaccatcaa caagcgcttc accaccggca cgcacctgaa 3660
245 gggcgtgtac ctgacacctga agagccagaa cggcgacgag gcctggggcg acaacttcat 3720
247 catcctggag atcagcccca gcgagaagct gctgagcccg gagctgatca acaccaacaa 3780
249 ctggaccagc accggcagca ccaacatcag cggcaacacc ctgaccctgt accagggcgg 3840
251 ccgcggcatc ctgaagcaga acctgcagct ggacagcttc agcacctacc gcgtgtactt 3900
253 cagcgtgagc ggcgacgcca acgtgcgcat ccgcaactcc cgcgaggtgc tggtcgagaa 3960
255 gaggtacatg agcggcgcca aggacgtgag cgagatgttc accaccaagt tcgagaagga 4020
257 caacttctac atcgagctga gccagggcaa caacctgtac ggcgggccga tcgtgcactt 4080
259 ctacgacgtg agcatcaagt aggagctcta gatccccgga atttccccga tcgttcaaac 4140
261 atttggcaat aaagtcttctt aagattgaat cctgttgccg gtcttgcat gattatcata 4200
263 taatttctgt tgaattacgt taagcatgta ataattaaca tgtaatgcat gacgttattt 4260
265 atgagatggg tttttatgat tagagtcctc caattataca tttaatcgc gatagaaaac 4320
267 aaaatatagc gcgcaaacta ggataaatta tcgcgcgcgg tgtcatctat gttactagat 4380
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272 <210> SEQ ID NO: 9
273 <211> LENGTH: 789
274 <212> TYPE: PRT
275 <213> ORGANISM: Artificial Sequence
277 <220> FEATURE:
278 <223> OTHER INFORMATION: VIP3A protein motif
280 <400> SEQUENCE: 9
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283 1 5 10 15
286 Ile Asp Tyr Phe Asn Gly Ile Tyr Gly Phe Ala Thr Gly Ile Lys Asp
287 20 25 30
290 Ile Met Asn Met Ile Phe Lys Thr Asp Thr Gly Gly Asp Leu Thr Leu
291 35 40 45
294 Asp Glu Ile Leu Lys Asn Gln Leu Leu Asn Asp Ile Ser Gly Lys
295 50 55 60
298 Leu Asp Gly Val Asn Gly Ser Leu Asn Asp Leu Ile Ala Gln Gly Asn
299 65 70 75 80
302 Leu Asn Thr Glu Leu Ser Lys Glu Ile Leu Lys Ile Ala Asn Glu Gln
303 85 90 95
306 Asn Gln Val Leu Asn Asp Val Asn Asn Lys Leu Asp Ala Ile Asn Thr
307 100 105 110
310 Met Leu Arg Val Tyr Leu Pro Lys Ile Thr Ser Met Leu Ser Asp Val
311 115 120 125
314 Met Lys Gln Asn Tyr Ala Leu Ser Leu Gln Ile Glu Tyr Leu Ser Lys
315 130 135 140
318 Gln Leu Gln Glu Ile Ser Asp Lys Leu Asp Ile Ile Asn Val Asn Val
319 145 150 155 160
322 Leu Ile Asn Ser Thr Leu Thr Glu Ile Thr Pro Ala Tyr Gln Arg Ile
323 165 170 175
326 Lys Tyr Val Asn Glu Lys Phe Glu Glu Leu Thr Phe Ala Thr Glu Thr
327 180 185 190
330 Ser Ser Lys Val Lys Lys Asp Gly Ser Pro Ala Asp Ile Leu Asp Glu
331 195 200 205
334 Leu Thr Glu Leu Thr Glu Leu Ala Lys Ser Val Thr Lys Asn Asp Val
335 210 215 220

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339 225                230                235                240
342 Asn Asn Leu Phe Gly Arg Ser Ala Leu Lys Thr Ala Ser Glu Leu Ile
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346 Thr Lys Glu Asn Val Lys Thr Ser Gly Ser Glu Val Gly Asn Val Tyr
347                260                265                270
350 Asn Phe Leu Ile Val Leu Thr Ala Leu Gln Ala Gln Ala Phe Leu Thr
351                275                280                285
354 Leu Thr Thr Cys Arg Lys Leu Leu Gly Leu Ala Asp Ile Asp Tyr Thr
355 290                295                300
358 Ser Ile Met Asn Glu His Leu Asn Lys Glu Lys Glu Glu Phe Arg Val
359 305                310                315                320
362 Asn Ile Leu Pro Thr Leu Ser Asn Thr Phe Ser Asn Pro Asn Tyr Ala
363                325                330                335
366 Lys Val Lys Gly Ser Asp Glu Asp Ala Lys Met Ile Val Glu Ala Lys
367                340                345                350
370 Pro Gly His Ala Leu Ile Gly Phe Glu Ile Ser Asn Asp Ser Ile Thr
371                355                360                365
374 Val Leu Lys Val Tyr Glu Ala Lys Leu Lys Gln Asn Tyr Gln Val Asp
375 370                375                380
378 Lys Asp Ser Leu Ser Glu Val Ile Tyr Gly Asp Met Asp Lys Leu Leu
379 385                390                395                400
382 Cys Pro Asp Gln Ser Glu Gln Ile Tyr Tyr Thr Asn Asn Ile Val Phe
383                405                410                415
386 Pro Asn Glu Tyr Val Ile Thr Lys Ile Asp Phe Thr Lys Lys Met Lys
387                420                425                430
390 Thr Leu Arg Tyr Glu Val Thr Ala Asn Phe Tyr Asp Ser Ser Thr Gly
391                435                440                445
394 Glu Ile Asp Leu Asn Lys Lys Lys Val Glu Ser Ser Glu Ala Glu Tyr
395 450                455                460
398 Arg Thr Leu Ser Ala Asn Asp Asp Gly Val Tyr Met Pro Leu Gly Val
399 465                470                475                480
402 Ile Ser Glu Thr Phe Leu Thr Pro Ile Asn Gly Phe Gly Leu Gln Ala
403                485                490                495
406 Asp Glu Asn Ser Arg Leu Ile Thr Leu Thr Cys Lys Ser Tyr Leu Arg
407                500                505                510
410 Glu Leu Leu Leu Ala Thr Asp Leu Ser Asn Lys Glu Thr Lys Leu Ile
411                515                520                525
414 Val Pro Pro Ser Gly Phe Ile Ser Asn Ile Val Glu Asn Gly Ser Ile
415 530                535                540
418 Glu Glu Asp Asn Leu Glu Pro Trp Lys Ala Asn Asn Lys Asn Ala Tyr
419 545                550                555                560
422 Val Asp His Thr Gly Gly Val Asn Gly Thr Lys Ala Leu Tyr Val His
423                565                570                575
426 Lys Asp Gly Gly Ile Ser Gln Phe Ile Gly Asp Lys Leu Lys Pro Lys
427                580                585                590
430 Thr Glu Tyr Val Ile Gln Tyr Thr Val Lys Gly Lys Pro Ser Ile His
431                595                600                605
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date